

GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds  
 (without alignments)  
 1537.035 Million cell updates/sec

Title: US-08-978-217-16

Perfect score: 1985

Sequence: 1 MAATCEISNVFSNFNAMS..... YKFGKNSSGKBEREVGESRN 371

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapekt 0.5  
 Ygapop 10.0 , Ygapekt 0.5  
 Fgapop 6.0 , Fgapekt 7.0  
 Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USP1Q_spool/US88978217/runat_14032003_141838_13457/app_query.fasta_1.1500
-DB=issued_patents_na -QFMT=factap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIXX=blosum62 -TRANS=human40.cdi
-LIST=5 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 THR MIN=0 ALIGN=15
-MODEL=LOCAL -QFMT=PTC -NORMext -HEAPSIZE=50000 -MINLEN=50 -MAXLEN=200000000
-USER=US88978217 @CGN 1 1_131 @runat_14032003_141838_13457 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_MMAPP -LARGEQUERY -NEG SCORES -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADD=1 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Issued Patents-NA:\*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTNS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/bactilesi.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1712	86.2	1920	1 US-08-746-782A-1
2	586	29.5	5427	Sequence 1, Appli
3	580	29.2	5510	Sequence 2, Appli
4	580	29.2	5667	Sequence 3, Appli
5	543	27.4	852	Sequence 4, Appli
6	543	27.4	852	Sequence 4, Appli
7	543	27.4	852	Sequence 4, Appli
8	543	27.4	852	Sequence 4, Appli
9	543	27.4	852	Sequence 4, Appli
10	543	27.4	852	Sequence 4, Appli
11	25.5	848	4 US-09-232-142A-44	Sequence 4, Appli
12	435.5	21.9	2280	3 US-09-009-913-8

Command line parameters:

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-DB=issued_patents_na -QFMT=factap -SUFFIX=rml -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIXX=blosum62 -TRANS=human40.cdi
-LIST=5 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 THR MIN=0 ALIGN=15
-MODEL=LOCAL -QFMT=PTC -NORMext -HEAPSIZE=50000 -MINLEN=50 -MAXLEN=200000000
-USER=US88978217 @CGN 1 1_131 @runat_14032003_141838_13457 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_MMAPP -LARGEQUERY -NEG SCORES -WAIT -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADD=1 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Issued Patents-NA:\*

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTNS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/bactilesi.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

##### RESULT 1

US-08-746-782A-1

; Sequence 1, Application US/08746782A

; Patent No. 5789200

##### GENERAL INFORMATION:

APPLICANT: Ismail Kola, Martin J. Tymms, Christine Debouck

TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3

##### NUMBER OF SEQUENCES: 4

##### CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
 SOFTWARE: MICROSOFT WORD

##### CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/746,789A,  
 FILING DATE: No. 5789200ember 15, 1996

CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: William T. Han

REGISTRATION NUMBER: 34,344  
 REFERENCE/DOCKET NUMBER: ATG 50024

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610 270 5219  
 TELEFAX: 610 277 4026

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:



Qy 27 AlaProAlaProProThrThr-----PheGlyThrGluAspLeuValLeuThr 42  
 |||| ::|||||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 84 GCTGCCCTCCCTCATGCCCAGCTATTGGATTCACCCAGATCTTGTGAA 140  
 Qy 43 LeuAsnAsnGlnGlnMetThrIleGluGly----- 52  
 |||:|||:|||:|||:  
 Db 141 -----ArgAGATCATGATCTGGAAAGGGTGGTAAATGAATCTAACCCGGCAAC 194  
 Qy 53 -----ProGluIysAlaserTPrThrSerGly----- 61  
 |||:|||:  
 Db 195 AACCTCTTCAAGCAGGCCAGCTGCAAGCACAGCAGCTACTCCACGGTCAATGTTCCAGT 254  
 Qy 62 -----ArgProGlnPheTrpSerLysThrGlnVal 71  
 |||:|||:  
 Db 255 GGGTTRTTGGAGGCCAGTGCGATGAAATTCTCATCCCTAGTACTGGCCAAGTACGGTG 314  
 Qy 72 LeuGluTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspPhe 91  
 |||:|||:  
 Db 315 TCGGAGTGGCTCAGAACGACCTCTGGACACCAGCTGGATGCCATTGATCCCTTC 374  
 Qy 92 SerArgCysAsnMetAspGlyValIleThrLeuCysSerCysAlaLeuGluGluLeuAspGlu 111  
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 Db 375 CAAAGCTGCACATCACGGCGACCTCTGGAGTAGTGGAGGTTGGAGGTCACCCGG 434  
 Qy 112 ValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAla--- 130  
 |||:|||:  
 Db 435 GGGCGAGGAGCCGGCGGCGACCTCCCTACAGCAACTTGCGACATCTGAAGTGGACGGC 494  
 Qy 131 -----SerSerAspGluLeuSerTrpIleSerIleGluLeuLeuGluLysAspGlyMetSer 148  
 Qy 495 CAGTGTAGTAGTGAC-----  
 Qy 149 PheGluGluLeuSerLeuGlyAspLeuGlyProPheAspGlySerProPheAlaGlnGlu 168  
 |||:|||:  
 Db 513 TTCCACTCCACACATGTCATGTGCAAGCTGAACTGAGCT-----TCC 563  
 Qy 169 LeuLeuAspAspGlyArgGlnAlaSerProTyTyCysSerThrTyGlyProGlyAla 188  
 ::|:|||:  
 Db 564 ATCATCACACCTGGAAAGACCAAGATAATTATAGACACCAACTATGGT----- 614  
 Qy 189 ProSerProGlySerSerAspValSerThrAlaArgThrAlaIleSerSerHis 208  
 |||:|||:  
 Db 615 -----ASGACA----- 620  
 Qy 209 AlaSerAspSerGlyGlySerAspValAspLeuThrGluSerLysValPhePro 228  
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 Db 621 -----GTAATGTTGACGCAACATTCTCTGTC 650  
 Qy 229 ArgAspAspPhe-----ThrAspPheLysGlyGluProLysHisGly 243  
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 Db 651 CGGGCTCAGATCTCCATGACAAACCAAGTCACCTCTGTGCAAGTCACCTGATG 710  
 Qy 244 LysArgLysAspArgLysGlyArgProArgLysLeuSerLysGluTyTrpAspCysLeuGluGly 263  
 |||:|||:  
 Db 711 AAAAGGAGCAAGACCCCTGCGAACGACACCAA----- 749  
 Qy 264 LysLysSerLysHisAlaProArgGlyThrHisLeuPheGluPheIleArgAspIleLeu 283  
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 Db 750 -----AGGACAAACCCGAGGAGGACTCTCTGGAAATCTACCGCGACATCTC 800  
 Qy 284 IleHisProGluLeuValGluGlyLeuMetLysTrpGluAspArgLysGluGlyValPhe 303  
 ::|:|||:  
 Db 801 TTGAAACCCAGAACGACCCAGATATAAATGCGAGACGCGATCTGGCGCTTC 860  
 Qy 304 LysPheLeuArgSerGluAlaValAlaGlnLeuPheGlyGlnLysLysLysAsnSerAsn 323  
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 Db 861 AGGTTCTGAAATCACAGGCACTGGCTCAGCTATGGCTAAATGAGACACAGAG 920  
 Qy 324 MetThrTyrglyluseuserargAlaMetArgTyryTyryTyryLysArgGluIleLeuGlu 343  
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 Db 921 ATGACCTATGAAAGCTCAGCGGAGCTATGAGATATCTACAAAGAGAAATCTCTGAG 980  
 Qy 344 ArgValAspGlyArgArgLysValTyrLysHeGlyLysAsnSerSerGlyTrpLysGlu 363  
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 Db 981 CCTGTGATGCGAAGACTGGTATAATTGGAAAGAATGCCGAGGAGGAGAA 1040  
 Qy 364 GluGlu 365  
 Db 1041 ATGAA 1046  
 RESULT 3  
 US-09-009-913-3  
 ; Sequence 3, Application US/09009913  
 ; Patent No. 608485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AXXY Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Asthma Related Genes  
 ; NUMBER OF SEQUENCES: 339  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bozicevic & Reed, LLP  
 ; STREET: 285 Hamilton Ave., Suite 200  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/009,913  
 ; FILING DATE: 21-JAN-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; PILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sherwood, Pamela J  
 ; REGISTRATION NUMBER: 36,677  
 ; REFERENCE/DOCKET NUMBER: SEQ-4P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-327-3231  
 ; TELEX:  
 ; MOLECULE TYPE: cDNA  
 ; DB: US-09-009-913-3  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5510 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-09-009-913-3  
 Alignment Scores:  
 Pred. No.: 1.16e-51. length: 5510  
 Score: 580.00. matches: 129  
 Percent Similarity: 54.43%. conservative: 43  
 Best Local Similarity: 40.82%  
 Qry Match: 29.22%  
 DB: 3  
 Gaps: 7  
 US-08-978-217-16 (1-371) x US-09-009-913-3 (1-5510)  
 Qy 58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyr 77  
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 Db 356 TCGCATGAAATCTATCCCTAGTACTGGCACAGTACCGAGGTTGGCTCCCGCAC 415  
 Qy 78 GluValGluLysAsnLysTyrAspAlaSerSerIleAspSerSerArgCysAsnMetAsp 97  
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 Db 416 CTCCTGGACACCAACGCTGGATCTGATCTCCCTTCAGAGTTGCGACATCAC 475  
 Qy 98 GlyAlaThrLeuCysSerCysAlaLeuGluLeuArgLeuValPheGlyProLeuGly 117  
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 Db 476 GCGGAGCACCTGAGCATGAGTTGGAGGTTACCCGGCGCAGGAGCGGGGGGG 535

QY 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSerAspGlu 134  
Db 536 CAGCTCCCTCTACAGCAACTTGAGCATCHGAACTGGCCAGTCAGTGC--- 592  
QY 135 LeuSerTriPleleGluleuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGly 154  
Db 593 -----CTGTCCAGTCCACACAAAT 613  
QY 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArg 174  
Db 614 GTCATGTCAGACTGAACTGAGCCT-----TCCCATGACACCTGGAA 664  
QY 175 GluAlaSerProTyrrTyrySerThrTrpGlyProGlyAlaProSerProGlySer 194  
Db 698 -----AGCACA-----  
QY 215 SerAspValAspLeuAspLeuThrGluSerLeuValPheProArgAspAspHe----- 232  
Db 704 -----GTAGATTGTTGAGCACAGCAACTTCTGCCGGCTCAGATCTCCATG 751  
QY 233 -----ThrAspTyryLysylGlyProLysHsGlyLysArgLysArgGlyArg 249  
Db 752 ACAACCAAGTCACCTCTCTGTCAGAGTCACCTGATAGTAAAAGGAGCAGACCCC 811  
QY 250 ProArgTyrySerLeuSerLysGluTyrrTrpAspCysLeuGluGlyLysLysSerLysBisala 269  
Db 812 CCTGCCAGTCCACACAA-----AAGCACAC 841  
QY 270 ProArgGlyThrHisLeuTrpGluPheIleArgAspLeuLeuHisProGluLeuAsn 289  
Db 842 CCAGAGGGACTCTTATGGAAATTCTACCGGCACATCTCTGAAACCAGAACAGAC 901  
QY 290 GluGlyLysMetLysTrpGluAsnArgLysGluLysValPheIysPhleuAsnSer 309  
Db 902 CCAGGATTAATAATGGAGGACCGTCTGAGGGCTTCAGGTCTTGAAATCAGG 961  
QY 310 AlaValAlaGlnLeuTrpGlyGlnLysLysLysSerAsnMetThrTyrGluLysIeu 329  
Db 962 GGAGGCGCTAGCTATGGCTAAKAGAGAACACAGGAGCACTGAAAGCT 1021  
QY 330 SerArgAlaMetArgTyrrTyrySerGluLeuGluGluGluValAspGlyArgArg 349  
Db 1022 AGCGGACTATGAGATATTACTACAAAGAGAACATCTGGCGCTGATGAGCAAGA 1081  
QY 350 LeuValTyrySerGlyLysSerArgTrpLeuGluGlu 365  
Db 1082 CCGTATATAATTGGGAGAGATGCCGGAGATGGAGANGAAATGAA 1129

RESULT 4  
US-09-009-913-4  
Sequence 4, Application US/09009913  
; Patent No. 6,087,485  
; GENERAL INFORMATION:  
; APPLICANT: AXYZ Pharmaceuticals, Inc.  
; TITLE: Method of Invention for Asthma Related Genes  
; NUMBER OF SEQUENCES: 339  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton Ave, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0

APPLICATION NUMBER: US/09/009,913  
FILING DATE: 21-JAN-1998  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sherwood, Pamela J  
REGISTRATION NUMBER: 36,677  
REFERENCE/DOCKET NUMBER: SEQ-4P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-327-3231  
TELEFAX: 650-327-3221  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5667 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: Linear  
MOLECULE TYPE: cDNA  
US-09-009-913-4  
Alignment Scores:  
Pred. No.: 1 21e-51 Length: 5667  
Score: 580.00 Matches: 129  
Percent Similarity: 54.43% Conservative: 43  
Best Local Similarity: 40.82% Mismatches: 78  
Query Match: 29.22% Indels: 66  
DB: 3 Gaps: 7  
US-08-978-217-16 (1-371) x US-09-009-913-4 (1-5667)  
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Db 513 TGGCATGAATTCTATCCCTCAGTACTGGACCAAGTACCAAGGTGTTGAGGAGTCACAC 572  
QY 78 GluValGluLysLysLysTyrAspDalaSerSerIleAspPheSerArgCysAsnMetAsp 97  
Db 573 CTCCCTGGACACCAACAGCTGGATGCCAATGTTGATCCCTTCCAGACTTGACATCAC 632  
QY 98 GlyValAlaThrLysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 117  
Db 633 GGCGGACACCTCTCCAGCATGAGTTGCGAGGTCACCGGGGGCAGGGACGGGGGG 692  
QY 118 AspGlnLeuHisAlaGlnLeuLeuGluSerAsn-----SerSerAspGlu 134  
Db 693 CAGCTCTCTACAGCAACTTGAGCATGAACTGAACTGGACGCCAGTGCACTGAC--- 749  
QY 135 LeuSerTriPleleGluleuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGly 154  
Db 750 -----CTGTCCAGTCCACACAAAT 770  
QY 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArg 174  
Db 771 GTCATGTCAGACTGAACTGAGCCT-----TCCATCATGACACCTGGAA 821  
QY 175 GluAlaSerProTyrrTyrySerThrTrpGlyProGlyAlaProSerProGlySer 194  
Db 822 GACGAGAACTTATTAATGACACCAACTATGGT----- 854  
QY 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGly 214  
Db 855 -----AGCACA----- 860  
QY 215 SerAspValAspLeuAspLeuThrGluSerLeuValPheProArgAspAspHe----- 232  
Db 861 -----GTAGATTGTTGAGCACAGCAAACTTCTGCCGGCTCAGATCTCCATG 908  
QY 233 -----ThrAspTyryLysLysGlyLysGluProLysHsGlyLysArgLysArgGlyArg 249  
Db 909 ACAACCAAGTCACCTCTCTGTCAGAGTCACCTGATGAAAGGAGCAAGACCCC 968





FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(852)  
 OTHER INFORMATION: n = A,T,C or G

US-09-605-785-44

Alignment Scores:  
 pred. No.: 5.98e-49  
 Score: 543.00  
 Percent Similarity: 54.28%  
 Best Local Similarity: 40.79%  
 Query Match: 27.36%

Db: 4 Gaps: 7

US-08-978-217-16 (1-371) x US-09-605-785-44 (1-852)

Qy 70 GlnValLeuGluTrpIleSerTyrGlnValGluLysAsnTyrAspAlaSerSerIle 89  
 Db 850 CAGGTCTGGGAGTGGCTCATCACCTCTGGACACCAACAGTGATGCCAATTGTAC 791

Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGlugIle 109  
 Db 790 CCTTCANGACTCCACATCACGGCGAGCACCTTGAGCATGAGTTGAGGAGTC 731

Qy 110 ArgLeuValPheGlyProLeuGlyArgAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129  
 Db 730 ACCCGGCCGGCAGGGACGGCGGCANCTCCCTACAGCAACTTGCGCATCTGAATGG 671

Qy 130 Asn-----SerSerAspGluLeuSerTrpIleGluLeuGluLysAspGly 146  
 Db 670 AACGCCAGTCAGTGTGAC----- 650

Qy 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProheAla 166  
 Db 598 ---CTGTCAGCAACCTGGAAAGACNAGACTTATTATGACAACACTGAGCT---- 599

Qy 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186  
 Db 649 ---TCCATCAGCAACCTGGAAAGACNAGACTTATTATGACAACACTGAGCT---- 545

Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 Db 544 -----AGCACA----- 539

Qy 207 SerHisAlaSerAspSerGlySerAspValAspLeuAspLeuThrGluSerLysVal 226  
 Db 538 -----GTAGATTGTGACAGCAAACT 515

Qy 227 PheProIleGlyAspAspPhe-----TheaPheTyrLysGlyGluLpPolys 241  
 Db 514 TCTGCGGGCTCAGAACCTCCATGACACCAACGTCACCTCTCTGTGAGTCCT 455

Qy 242 HisGlyLysBglLysSerLysBglLysBglLysSerLysBglLysGluThrTyrTrpAspCysLeu 261  
 Db 454 GATATGAAAGGAGAACGCCCTGGCCAGTGCACACCAA----- 410

Qy 262 GluGlyLysBglLysSerLysBglLysBglLysSerLysBglLysGluThrLeuAspGly 281  
 Db 409 -----AGCACACCCGAGAGGACTACTATGGAAATTCTCCGGAC 365

Qy 282 IleLeuIleLeuAspProGluLeuAspGluLysLeuMetLeuTyrGluLeuAspGly 301  
 Db 364 ATCCCTCTGAAACCAAGACAAGACCAACGAGATTATAAATGGGAAACGGCTCTGAGGGC 305

Qy 302 ValPhenLysPheLeuArgSerGluLysValAlaGlnLeuTrpGlyGlnLysLysLysAsn 321  
 Db 304 GTCTTAGGTTCTGAAATCACAGGGAGGGCTGCTCACTGGTAAAGAGAAC 245

Qy 322 SerAspMetThrTyrglyIleLeuSerArgAlaMetArgTyryTyryTyryArgGluLys 341  
 Db 244 ACCAGATGACCTATGAAAGCTCAGCGGAGCTATGAGATATACTACAAAGAGAAATT 185

Qy 342 LeuGluLysValAspGlyArgArgLeuValTyrLysPheGlyLysAsnSerSerGlyTyr 361

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RESULT 8  
 US-09-439-313-44/c  
 Sequence 44, Application US/09439313  
 Patent No. 6329505  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer L.  
 APPLICANT: Jiang Yuqui  
 APPLICANT: Rettner, Mark  
 APPLICANT: Reed, Steven G.  
 APPLICANT: Kalos, Michael  
 APPLICANT: Ranger, Gary  
 APPLICANT: Solk, John  
 APPLICANT: Day, Craig  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 FILE REFERENCE: 210121-427C9  
 CURRENT APPLICATION NUMBER: US/09/439,313  
 NUMBER OF SEQ ID NOS: 575  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 44  
 LENGTH: 852  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE: misc\_feature  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(852)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-439-313-44

Alignment Scores:  
 pred. No.: 5.98e-49  
 Score: 543.00  
 Percent Similarity: 54.28%  
 Best Local Similarity: 40.79%  
 Query Match: 27.36%

Db: 4 Gaps: 7

US-08-978-217-16 (1-371) x US-09-439-313-44 (1-852)

Qy 70 GlnValLeuGluTrpIleSerTyrGlnValGluLysAsnTyrAspAlaSerSerIle 89  
 Db 850 CAGGTCTGGGAGTGGCTCATCACCTCTGGACACCAACAGTGATGCCAATTGTAC 791

Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGlugIle 109  
 Db 790 CCTTCANGACTCCACATCACGGCGAGCACCTTGAGCATGAGTTGAGGAGTC 731

Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129  
 Db 730 ACCCGGCCGGAGGGACGGCGGGCANCTCTACAGCAACTTGAGCATCTGAATGG 671

Qy 130 Asn-----SerSerAspGluLeuSerTrpIleGluLeuGluLysAspGly 146  
 Db 670 AACGCCAGTCAGTGTGAC----- 650

Qy 147 MetSerPheGlnGluSerLeuGlyAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186  
 Db 649 ---CTGTCAGCCACACATGTCATGTCAGACTGACAACTGAGCT---- 599

Qy 167 GlnGluLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186  
 Db 598 ---TCCATCAGCAACCTGAAAGACNAGACTTATTATGACCAACTATGCT---- 545

Query / Match: 27.36% Indels: 66 Gaps: 7

DB: US-09-978-217-16 (1-371) x US-09-352-616A-44 (1-852)

Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206

Db 544 -----|||-----AGCACA----- 539

Qy 207 SerHisAlaSerAspSerGlyGlySerAspValAspleusAspleuThrGluSerIysVal 226

Db 538 -----|||-----GTTGATGGTGCACTGACAACT 515

Qy 227 PheProArgAspAspPhe-----ThrAspTyrLysLysGlyGluProlys 241

Db 514 TCTGCCGGCTCATGACAAACCAAGTCAGTCACCTCTGTGAGTCAGAGTCACCT 455

Qy 242 HisGlyLySArgLysBargLysProArgLysLeuSerIysGluTyrrTrpAspCysLeu 261

Db 454 GATATGAAAAGGAGCAAGACCCCTGCGCAAGGCCACACAA 410

Qy 262 GluglyLysLysSerLysSerHisAlaProArgLysThrHisLeuTrpLysLysLeu 281

Db 409 -----|||-----AAGCACACCCGAGGACTCTACTTAATGGAACTGCGAC 365

Qy 282 IleLeuIleHisProGluLeuAspGluGlyLeuMetLysTrpGluAsnArgLysGluGly 301

Db 364 ATCCCTCTGAACCCAGACAGAACCCAGGTTAAATGGAAAGCCGATCTGGGC 305

Qy 302 ValPhelysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGluLysIysAsn 321

Db 304 GTCCTCAGGTTCTGAAATGAGGCACTGAGCTAGCTAGGGTAAAGAGACAC 245

Qy 322 SerAspMetThrTygIlysLeuSerGalaMetAspTytyTytyLysBargLile 341

Db 244 AGCACATGACCATTGAAAGCTCAGGCCAGCTATGAGATATACCAAGAACATT 185

Qy 342 LeuGluArgValAspGlyArgArgLeuValTyryLysPhGlyLySAsnSerSerGlyTriP 361

Db 184 CTGGAGCGTGTGGATGGAGAAGACTGGTATAATTGGAGAATGCCGAGGATGG 125

Qy 362 LysGluGluGlu 365

Db 124 AGAGAAATGAA 113

RESULT 9

US-09-352-616A-44/c

; Sequence 44, Application US/09352616A

; Patient No. 639578

; GENERAL INFORMATION:

; APPLICANT: Dillon, Davin C.

; APPLICANT: Harfocker, Susan Louise

; APPLICANT: Jiang, Yuqui

; APPLICANT: Xu, Jiaochun

; APPLICANT: Mitcham, Jennifer Lynn

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121\_427C8

; CURRENT APPLICATION NUMBER: US/09/352,616A

; CURRENT FILING DATE: 1999-07-13

; NUMBER OF SEQ ID NOS: 472

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 44

; LENGTH: 852

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE: NAME/KEY: misc\_feature

; LOCATION: (1)..(852)

; OTHER INFORMATION: n = A,T,C or G

US-09-352-616A-44

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:
543.00	54.28%	852	124	41	73
40.79%					

Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109

Db 790 CCTTTCACAGTGTGACATCAAGGGAGCACCTTGAGCATGAGTTCAGAGTC 731

Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuLysIleAlaGlnLeuArgAspLeuThrSer 129

Db 730 ACCCGCCGCCAGGGACGGCGGGGACNTCTCTACGAACTTCAGCATCTGAGTGG 671

Qy 130 Asn-----SerSerAspGluLeuSerTrpIleLleGluLeuIleGluLysAspGly 146

Db 670 AACGCCAGTCAGTAGTCAC 650

Qy 147 MetSerPheGlnGluSerIeUGlyAspLeuGlyProPheAspGlnGlySerProHeAla 166

Db 649 ---CCTCTCAGTCACACACAATGTCATGTCAGACTGAACTGAGCT---- 599

Qy 167 GluGluLeuAspAspGlyYatGQInAlaSerProTyrrTyrcysSerThrTyrglyPro 186

Db 598 ---TCATCATGAAACACTGAAAGACAGNAGACTTATGACCAACTATGT--- 545

Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206

Db 544 -----|||-----AGCACA 539

Qy 207 SerHisAlaSerAspSerGlyGlySerAspValAspleuAspleuThrGluSerIysVal 226

Db 538 -----|||-----GTTGATGGTGCACTGACAACT 455

Qy 227 PheProArgAspAspPhe-----ThrAspTyrLysLysGlyGluProlys 241

Db 514 TCTGCCGGCTCATGCAACCAAGCTCCGCAAGCCCACCAAA 410

Qy 242 HisGlyLySArgLysBargLysProArgLysLeuSerIysGluTyrrTrpAspCysLeu 281

Db 409 -----|||-----AAGCACACCCGAGGACTCTACTTAATGGAACTGCGAC 365

Qy 282 IleLeuIleHisProGluLeuAspGluGlyLeuLysTrpGluAsnGluGly 301

Db 364 ATCCCTCTGAACCCAGACAGAACCCAGGTTAAATGGAAAGCCGATCTGGGC 305

Qy 302 ValPhelysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysIysAsn 321

Db 304 GTCTCTAGGTTCTGAAATGAGCCAGCTCTGAGCTCTGAGCTATGAGATTCAC 245

Qy 322 SerAspMetThrTygIlysLeuSerAspGalaMetArgTyrrTytyLysBargLile 341

Db 244 AGCACATGACCATTGAAAGCTCAGGCCAGCTAGAGATATTACAAAGAACATT 185

Qy 342 LeuGluArgValAspGlyArgArgLeuValTyryLysPhGlyLySAsnSerSerGlyTriP 361

Db 184 CTGGAGCGTGTGGATGGAGAAGACTGGTATAATTGGAGAATGCCGAGGATGG 125

Qy 362 LysGluGluGlu 365

Db 124 AGAGAAATGAA 113

RESULT 10

US-09-232-149A-44/c

; Sequence 44, Application US/09232149A

; Patent No. 665611



Percent Similarity: 52.70%      Conservative: 39  
 Best Local Similarity: 39.53%      Mismatches: 84  
 Query Match: 3 5.54%      Index: 56  
 DB: Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-338 (1-848)

QY 56 AlaserTrpThrSerGluargProGlnPheTrpSerlylSthrGlnValLeuGluTrpIle 75  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 118 AGCCAGTCGGCATGAATCCACCTCTAGACTGGACAAATAACAGGTGGGATGGCT 177  
 QY 76 SerTyrGlnValGluLysAsnLyvTyraPalaSerSerSerIleAspPheSerArgCysAsn 95  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 178 CAGGCCTCTGGACACCAACAGCTAGCCTACTGGATCCCTTCAGGAGTCGC 237  
 QY 96 MetAspGlyValAlaThrLeuIleCysSerCysAlaLeuGluIleLeuArgLeuValPheGlyPro 115  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 238 ATTAGCGGGACACCTGTCAGCTGAGCTGAGCTGAGCTGAGGTCA 297

QY 116 LeuGlyAspGlnLeuHisAlaGlnLeuIleGluAspLeuThrSerAla 132  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 298 GCTGGGCACCTGCTCTACANGCAACCTACAGCATCTCAACTGGACGGCCAATCGAGCT 357  
 QY 133 AspGluLeuSerTrpIleLeuGluLeuLeuGluLeuAspGlyMetSerPheGlnGluSer 152  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 358 GAC-----CTTTCCAGTCGCCA 375

QY 153 LeuGlyAspIleGlyProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspasp 172

Db 376 CACAGTCATGTCAGCTGAGCTGACAAACCGATCT-----TCATCATCACACA 426

QY 173 GlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGly 192  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 427 TGGAAAGAAGAAAATCTCTATGATCCAGCTATGGTAGCTAGTAGATCTGTGGAC 486

QY 193 SerSerAspValSerThrAlaArgThrAlaThrProGlnSerHisAlaSerAspSer 212  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 487 AGTAAGACTTCTGCCGGCTAGTCATGACAACTCCAGTCAC----- 534

QY 213 GlyGlySerAspValAspLeuAspLeuThrGluSerValPheProArgAspPhe 232  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 535 -----CTTCACTGAGAGTC----- 552

QY 233 ThrAspTyrIleGlyGlyGluProLysHisGlyLysArgGlyArgProArgLys 252  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 553 CCTGATATGAAAG---GAGCAAGACACCT----- 582

QY 253 LeuSerLysGluTrpAspCysLeuGluGlyLysLysSerIleHisAlaProArgLys 272  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 583 -----GTAAGTCCCACACAAAGCACACACCAAGAGC 618

QY 273 ThrHisLeuTrpGluIlePheIleArgAspIleLeuIleIleProGluLeuAsnGluGlyIle 292  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 619 ACTCTTATGGAGTCCTCCGAGACATCTCTTGAGCCAGAACGACGGGCTG 678

QY 293 MetLysTrpGluAlaArgIleGluGlyValPheIysPheLeuArgSerCluAlaValAla 312  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 679 ATCAAATGGCAAGACCGTCTGGAAAGGCATCTTCAGGTCTCTGAAGTCAGCTGCT 738

QY 313 GluIleTrpGlyGlnIleGlyLysLysLysAsnSerAsnMetThrTyrGluLysIleSerArgAla 332  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 739 CAGCTGTGGGAAAGAAAGAAATPACGTCAGCTGACATAGAGGAAGTCACGGGGCT 798

QY 333 MetArgTyrIleGlyArgIleLeuGluIleLeuGluAspGlyArg 348  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 799 ATGAGATATTACTAQAACGAGAMTCCTGAGCTGGTGTGATGGCGA 846

TITLE OF INVENTION: Asthma Related Genes  
 NUMBER OF SEQUENCES: 339  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Boicevic & Reed, LLP  
 STREET: 205 Hamilton Ave, Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,913  
 FILING DATE: 21-JAN-1998  
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEFAX: 650-327-3231

TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2280 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-009-913-8

Alignment Scores:

Pred. No.: 8.91e-37

Score: 43.50

Percent Similarity: 46.60%

Best Local Similarity: 30.74%

Query Match: 21.94%

DB: 3

Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-8 (1-2280)

QY 58 TrpThrSerGluargProGlnPheTrpSerlylSthrGlnValLeuGluTrpIleSerTyr 77  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 206 TGGACATCTGTCACCTCTAACATCTGGACTAAGCTAACGGCCATGTTGGAGCTGGCTTCAGTC 265

QY 78 GluValGluLysAsnLyvTyraPalaSerSerSerIleAspPheSerArgCysAsnMetAsp 97  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 266 TGCTGCGACCAGTCACAGTTGACACCAATTCTCTCTGCAACTCACATG 325

QY 98 GluAlaThrLeuIleCysSerCysAlaLeuGluLeuIleArgLeuValPheGlyIleoleGly 117  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 326 GGCTGCGAGCTGTCAGCATGAGACACAGGAGGTTGCGAGCGACCTGGCTCTGCGGC 385

QY 118 AspGlnLeuHisAlaGlnLeuIleAspLeuThrSerAsnSerSerAspGluLeuSerTrp 137  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 386 GAGAACCTGCTAC----- 400

QY 138 IleLeuGluLeuIleGluGlyLysAspGlyMetSerPheGlnGluLeuIleLeuArgGlyIle 157  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 401 ATCCCTCCAGAACATCCGCAACACAGTTACTCTTT----- 436

QY 158 ProPheAspGlnGlySerProPheAlaGlnGluLeuAspaspGlyArgGlnAlaSer 177  
 :::: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 437 -----TTTAACTGACGTGAAAGAAAG 460

GENERAL INFORMATION:

APPLICANT: AxyS Pharmaceuticals, Inc.

RESULT 12

US-09-009-913-8

Sequence 8, Application US/09009913

Patent No. 6087485

GENERAL INFORMATION:

APPLICANT: AxyS Pharmaceuticals, Inc.

Db 461 ||||| GCCACCATCAAAGACTATGCTGATTCAC 490  
 Qy 198 ThrlAlargThrAlaThrProGlnSerSerHisAlaSerAspSerGlyLysLeuAspVal 217  
 Db 491 TGCTTGAAACAGTGCATCAAACTCAA 520  
 Qy 218 AspleuAspleuThrCluSerLysValPheProArgAspAspSerThrAspTyrLys 237  
 Db 520 ----- 520  
 Qy 238 GlyGluProLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyr 257  
 Db 520 ----- 520  
 Qy 258 TrpAspCysLeuGluGlyLysSerLysHisAlaProArgGlyLysLeuAspVal 277  
 Db 521 ---GAGCTG-----CACAGTCATAAGCTAACGCTCCAAAGTCTCACTATGGAA 571  
 Qy 278 PhelIargAspIleLeuIleHisProGluLeuAspGluGlyLeuMetLysTrpGluAsn 297  
 Db 572 TTGCTGAGACCTGCTCTCTGAAACACTGGCATCTGGATGGAGAT 631  
 Qy 298 ArgHisGluGlyValPhelAlaProArgGlyLysLeuAspVal 317  
 Db 632 AGGGAAACAAGGATTTCGGGTGTTAATCGGAAAGCCCTGGCAAGATGGGACAA 691  
 Qy 318 LysLysLysAsnSerAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyr 337  
 Db 692 AGGAACAAATGACAGAATGAGCTGAGTGAAGTGTGAGCAGCCCTGAGACTCTAT 751  
 Qy 338 LysArgGluIleLeuGluArgValArgLysLeuValTyrLysPheGlyLysAsn 357  
 Db 752 AAACCGGAATTGAGCGGGTGTAC---CGAAGGTAGTGACAAATTGGAAATA 808  
 Qy 358 SerSerGlyTrpLysGluGluIluVal 366  
 Db 809 GCACACGGTGGCAGGAGACAGCTTA 835

RESULT 13

US-09-009-913-6  
 ; Sequence 6, Application US/09009913  
 ; Parent No. 6057485

GENERAL INFORMATION:

APPLICANT: AXYX Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Asthma Related Genes  
 NUMBER OF SEQUENCES: 339  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bozicovic & Reed, LLP  
 STREET: 285 Hamilton Ave, Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913  
 FILING DATE: 21-JAN-1998  
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J  
 REGISTRATION NUMBER: 36 677  
 REFERENCE/DOCKET NUMBER: SEQ-4P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-322-3231  
 TELEFAX: 650-327-3231

INFORMATION FOR SEQ ID NO: 6 :

SEQUENCE CHARACTERISTICS:

LENGTH: 2428 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLogy: linear

MOLECULE TYPE: cDNA

US-09-009-913-6

Alignment Scores:

Pred. No.:	Score:	Length:
	9.82e-37	2428
	435.50	Matches: 95
	46.60*	Conservative: 49
	30.74%	Missmatches: 66
	21.94%	Indels: 99
DB:	3	Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-6 (1-2428)

Qy 58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyr 77  
 Db 354 TGCACATCAGCACCCTGAATACTGGACTAGCTAGGCCATCTGGGAGTGCCCTCCAGTC 413  
 Qy 78 GlnValGluLysAsnLysTyrAspLaseSerSerIleAspHeserArgCysAsnMetAsp 97  
 Db 414 TCTGCGACCACTACAGTGTGACACCAATTGCACTTCCTCTGCACACTCACAGTCAGT 473  
 Qy 98 GlyAlaThrIleCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 117  
 Db 474 GGCCTCGAGCTGCGCATGACACAGGGTGTGCTGAGCTGGCCCTCNGGG 533  
 Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTrp 137  
 Db 534 GAGTACCTGTAC----- 548  
 Qy 138 IleIleGluLeuIleGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspIeuGly 157  
 Db 549 ATCTCCAGAACATCGCACACAGGTACTCTT----- 584  
 Qy 158 ProPheAspGlyGlySerProPheAlaGlnLeuLeuLeuAspAspGlyArgGlnAlaSer 177  
 Db 585 -----TTTATGACCTGAGAAAGCAAG 608  
 Qy 178 ProTyrTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValser 197  
 Db 609 -----GCCACCATCAAAGACTATGCTGATTCAC 638  
 Qy 198 ThrlAlargThrAlaThrProGlnSerSerHisAlaSerAspSerGlyLysSerAspVal 217  
 Db 639 TCTTGAAACAGTGCATCAAACTCAA 668  
 Qy 218 AspleuAspleuThrCluSerLysValPheProArgAspAspSerThrAspTyrLys 237  
 Db 668 ----- 668  
 Qy 258 TrpAspCysLeuGluGlyLysSerLysHisAlaProArgGlyLysLeuSerLysGluTyr 257  
 Db 669 ---GAGCTG-----CACAGTCATAAGCTAACGCTCCAAAGTCTCACTATGGAA 719  
 Qy 278 PhelIargAspIleLeuIleHisProGluLeuAspGluGlyLeuMetLysTrpGluAsn 297  
 Db 720 TTGCTGAGACCTGCCTCTCTGGAAGAAACTGTGCGCATCTGGATGGAGAT 779  
 Qy 298 ArgHisGluGlyValPhelAlaProLeuAspSerGluAlaValAlaGlnLeuTrpGlyGln 317  
 Db 780 AGGGAAACAAGGATTTCGGGTAAATCGGAAAGCCCTGGCAAGATGGGGACAA 839  
 Qy 318 LysLysLysAsnSerAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyrTyr 337

Db 840 AGGAGAAGAAATGACAGAATGACTGAAGTGGAGAGCCCTGAGATCAT 899  
 Qy 338 LYARGGILleuLeugluArgValAspGlyArgLeuValTyrLysPheGlySer 357  
 Db 900 AAAACGGAATTGAGCGGTGAC---CGAAGTTGTAACAAATTGCAAAAT 956  
 Qy 358 SerSerGlyTrpLySgluGluVal 366  
 Db 957 GCACACGAGTCAGGAAGACAAGCTA 983

RESULT 14

US-09-009-913-10  
 Sequence 10, Application US/09009913  
 Patent No. 6087485  
 GENERAL INFORMATION:  
 APPLICANT: Axs Pharmaceuticals, Inc.  
 TITLE OF INVENTION: Asthma Related Genes  
 NUMBER OF SEQUENCES: 339  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bozicevic & Reed, LLP  
 STREET: 285 Hamilton Ave, Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009, 913  
 FILING DATE: 21-JAN-1998  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sherwood, Pamela J  
 REGISTRATION NUMBER: 36,677  
 REFERENCE/DOCKET NUMBER: SEQ-4P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-327-3231  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2498 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA.

US-09-009-913-10

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
1	435.50	46.60%	30.74%	21.94%	3
					Gaps:

US-08-978-217-16 (1-371) x US-09-009-913-10 (1-2498)

Qy 58 TRPThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyr 77  
 Db 423 TGCACATCAGTCACCTGAACTGCTAAAGGCCATGTRGGACTGGCCAGTC 482  
 Qy 78 GluValGluLysAsnLysTyrAspAlaSerSerLeAspHeserArgCysAsnMetAsp 97  
 Db 483 TGGTGCGACGAGCAGTGGACACCAATTGCACTCTCTGCAACTCAGATCAGT 542

Qy 98 GlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGly 117  
 Db 543 GGCCTGAGCTCTGAGCATGAGCACAGGAGGTTCTCGAGCCAGCTGGCTCTGGGG 602  
 Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyr 137  
 Db 603 GAGTACCTGTAC----- 617  
 Qy 138 IleLeuGluLeuLeuGluLysLysPheGlyMetSerPheGlnGluSerLeuGlyAspLeuGly 157  
 Db 618 ATCCTCCGAAATCCGACACAGGTACTCTT----- 653

Qy 158 PropheAspGlnDlySerProheAlaGlnGluLeuAspAspGlyArgGlnAlaSer 177  
 Db 654 -----TTAACGACGCTGAGAAAGCAAC 677

Qy 178 ProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValser 197  
 Db 678 -----GCACACCTCAAAGACTATGCTATCCAC 707

Qy 198 ThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGlySerAspVal 2117  
 Db 708 TGTTGAAACAGTGGCATCAAAGCTA----- 737

Qy 218 AspIleuAspLeuIhrGluSerLysValPheProArgAspAspPheThrAspTyrLys 237  
 Db 737 ----- 737

Qy 238 GlyGluProLySHisGlyLysArgLySArgGlyArgProArgLySLeuSerLysGluTyr 257  
 Db 738 --GACTCT-----CACAGTOATAAGAACAAGCTCCAAAGTTCATCTATGGAA 788

Db 737 ----- 737

Qy 258 TrpAspCysLeuGluGluLysLysSerLysIleProArgGlyLysIleLeuTrpGlu 277  
 Db 789 TTGTACGAGACCTGCCTCTATCTCTGAAAGAACTCTGGATTCGGAATGGGAGAT 848

Qy 298 ArgGlyGluGlyValPhelYsPheLeuArgSerGluLavalAlaGlnLeuArgLysGlu 317  
 Db 849 AGGGACAGGAAATTGCGGTTAAATGGAAGCTCGCAAGATGGGGCAA 908

Qy 318 LysLysLysAsnSerAsnMetThrTyrGlyLysLeuSerArgAlaMetArgTyrTyr 337  
 Db 909 AGCAAGAAAGAAATGACAGATGAGCTGAGTGAAGAATGAGCAGGCCCTGAGATACTAT 968

Qy 338 LYARGGILleuLeugluArgValAspGlyArgLeuValTyrLysPheGlyLysAsn 357  
 Db 969 AAAACGGAATTGAGCGGGTTGAC---CCAGGTTAGTGTACAAATTGCAAAAT 1025

Qy 358 SerSerGlyTrpLySgluGluVal 366  
 Db 1026 GCAACGGGTGCGAGGAGACAGCTA 1052

RESULT 15

US-08-308-281-1  
 Sequence 1, Application US/08368281  
 Patient No. 572113  
 GENERAL INFORMATION:  
 APPLICANT: Libermann, Towa A  
 APPLICANT: Oettgen, Joerg P  
 APPLICANT: Kunsch, Charles A  
 TITLE OF INVENTION: NERF Genes  
 NUMBER OF SEQUENCES: 9  
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